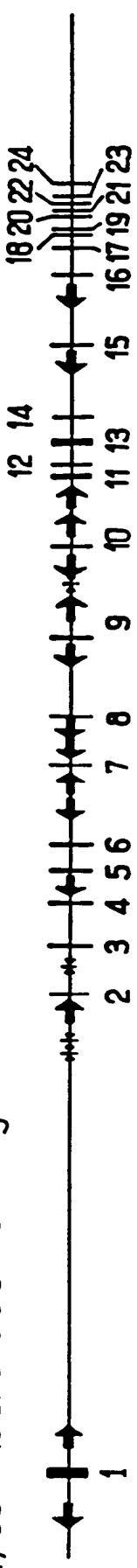
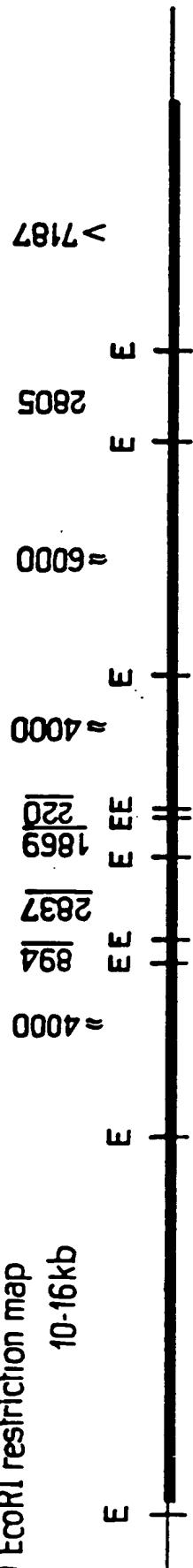


FIG. 1

A) Genomic structure of the nCL1 gene

B) EcoRI restriction map  
10-16 kb

C) Cosmid map

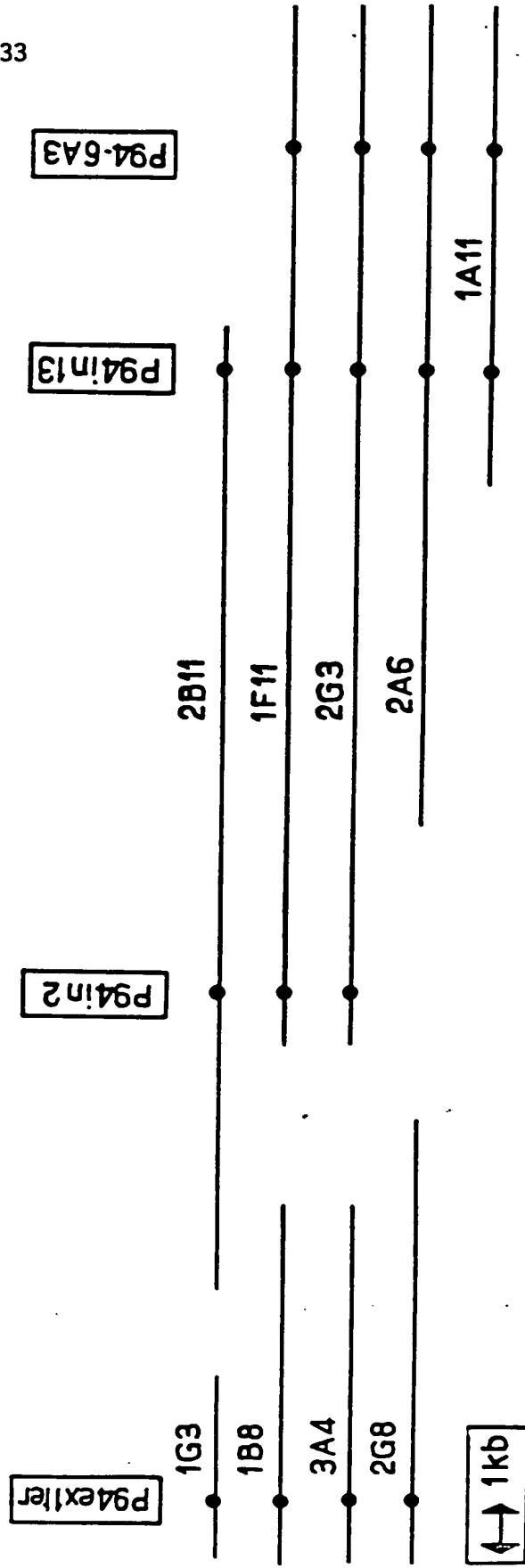


FIG. 2A

**FIG. 2B/1**

1 ATGCCGACCGTCATTAGGGCATCTGGCTCCAGGACAGGGCTGAGCCCGTCCCAGGGCCAGTTCCACCCCCAGCAAGGCACTGAGCTGCCGATGGCAAACTCCAGT  
 M P T V I S A P R T A E P R S P G P V P H P A Q S K A T E A C G C N P S 110  
 130 \* 150 170 190 210 230  
 G I Y S A I S R N F P I C V K E K T F E Q L H K K C L E K K V L Y V D P E F  
 250 270 290 310 330 350  
 CCACCGGATGAGACCTCTCTTATGCCAGAGCTTCCAGTCAAGAACATTGGACTTCAAGAAATGTGCTTAGAAAGAAGAGTCTTATGGACCCCTAGCTTC  
 P P D E F S L F Y S Q K F P I Q F V W K R P P E I C E N P R F I I D C A N R T D 370  
 370 390 410 430 450 470  
 ATCTGTCAGGAGACTTAAGGACTCTCTCTTATGCCAGAGCTTCCAGTCAAGAACATTGGACTTCAAGAAATGTGCTTAGAAAGAAGAGTCTTATGGAAACTACCGA  
 I C Q G E L C D C W F L A A I A C L T L N Q H L L F R V I P H D Q S F I E N Y A 490  
 490 510 530 550 570 590  
 GGATCTTCACCTCCAGGACTCTCTGGCTGGTTTCGAGCCATTGGCTGACCCATACCCCATGATCHAGCTTCAACTGGCTTTCACCLAGTCGAATGGTTC  
 G I F H F Q F W R Y C E W V D V V I D D C L P T Y N N Q L V F T K S N H R N E F 610  
 610 630 650 670 690 710  
 TCCAGTGTCTGCTGGAGAGGGCTTATGCTTAAGCTTCAGAACCTTGAGGACTGGCTGGCTTATAGATGACTGGCTGGCTTCAACTGGCTTTCACCCGAATGGTTC  
 W H S A L L E K A Y A K L H C S Y E A L K C G N T T E A H E D F T G C V A E F F E 730  
 730 750 770 790 810 830  
 ATCAGGGATGCTCTAGTACATGTACAGATCATGAAAGCAGGCTCTCATGGCTGGCTCCATTGAGGACTTCAAGGGCTTCAACTGGCTGGCTTCAACTGGCTGGCT  
 I R D A P S D M Y K I H K K A I E R G S L H C C S I D D G T N H T Y G T S P S C 850  
 850 870 890 910 930 950  
 CTGAAACATGGGGAGTTGACCGATAACTCTGCTAACCAAATATGGATAACTCTGCTGGCTCCATTGAGGACTCTGCTGGCTCCATTGAGGACTTCAACTGGCTGGCT  
 I L N H C E L I A R H V R N H D N S I L O D S D I D P R G S D E R P T R T I I P V 970  
 970 990 1010 1030 1050 1070  
 CAGTATGAGACAGCATGGCTGGCTGGCTGGCTCACAGGTACGGCTACTCTGCTAACCCCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT  
 Q Y E T R H A C G L V R G H A Y S V T C L D E V P F K C E K V K L V R L R N P W 1090  
 1090 1110 1130 1150 1170 1190  
 GGCCTGGCTGGACTGGACGGCTCTGGCTGGCTCACAGGTACATGGAAAGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT  
 C Q V E W N G S W S D R W K D W S F V D K D E K A R L Q H Q V T E D G E F W H S 1210  
 1210 1230 1250 1270 1290 1310  
 TATCAGGATTTCATTCACATTTCACAGATTGGAGATCTGGAACTCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT  
 E D F I Y H F T K L E I C N L T A D A L Q S D K L Q T W F V S V M E G R W V R

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PCT/EP95/04575

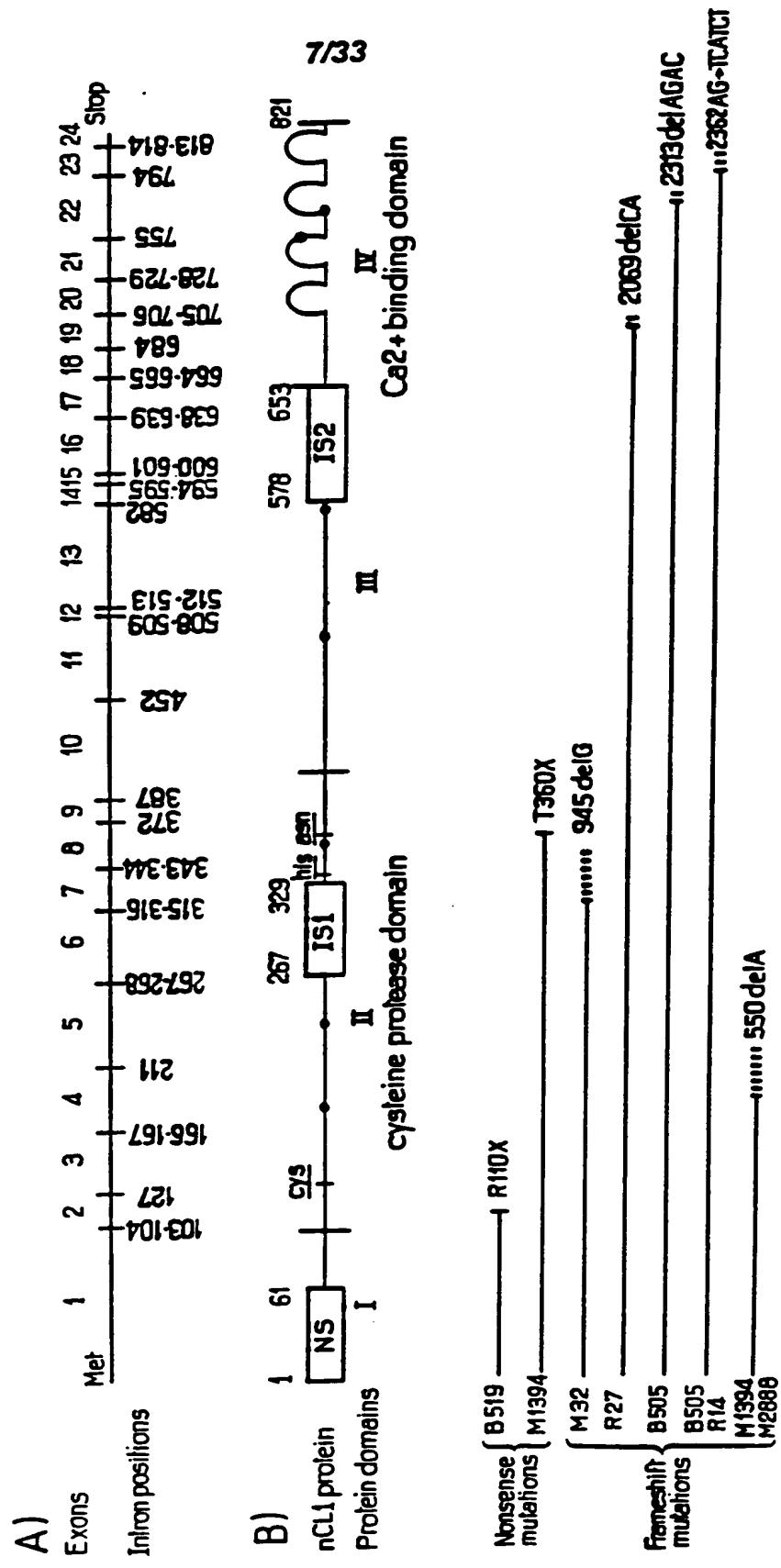
**FIG. 2B/2**

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**FIG. 2C**

## **SUBSTITUTE SHEET (RULE 26)**

**Figure 3:**

FIG. 4

SUBSTITUTE SHEET (RULE 26)

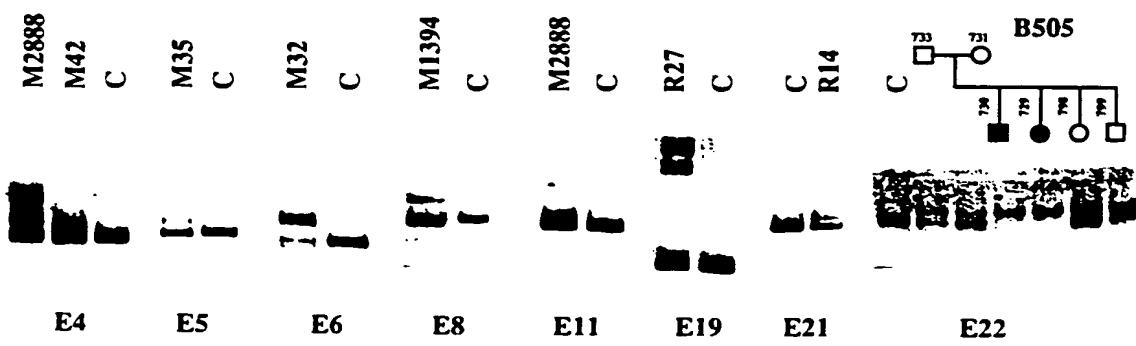
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heart  
brain  
placenta  
lung  
liver  
skeletal muscle  
kidney  
pancreas

**3.6 kb -**

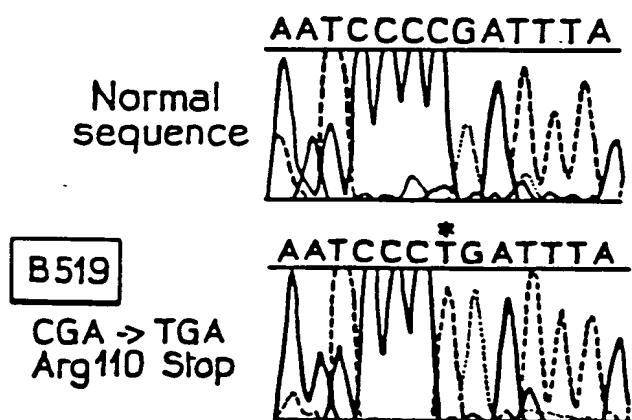
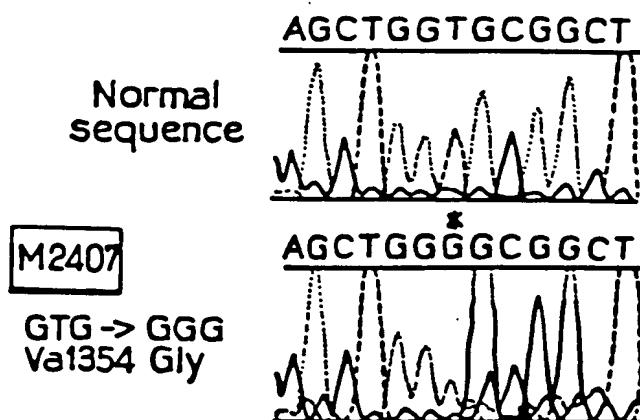
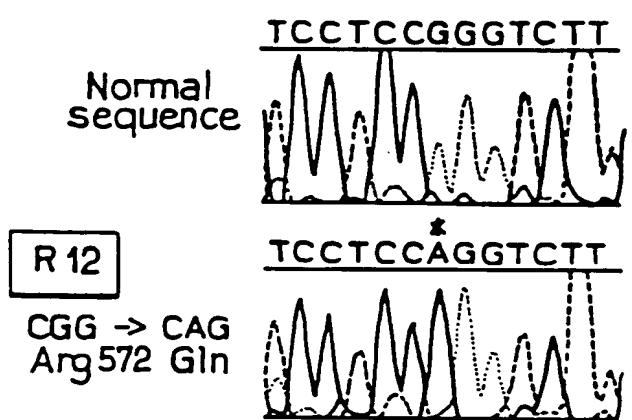
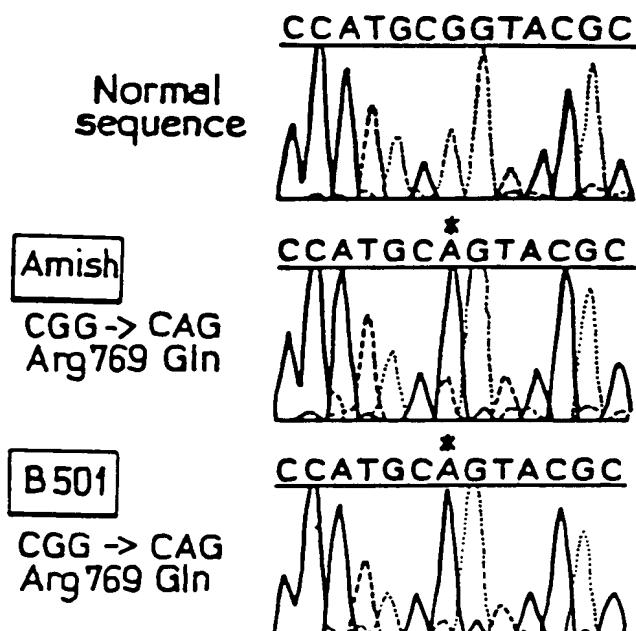
**FIG. 5**

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**FIG. 6**

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FIG. 7A) EXON 2B) EXON 8C) EXON 13D) EXON 22

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## LISTE DE SEQUENCES

## (1) INFORMATION GENERALE:

## (i) DEPOSANT:

- (A) NOM: AFM
- (B) RUE: 13, place de Rungis
- (C) VILLE: PARIS
- (E) PAYS: FRANCE
- (F) CODE POSTAL: 75013
- (G) TELEPHONE: (1) 45 65 13 00

## (ii) TITRE DE L' INVENTION: LGMD GENE

## (iii) NOMBRE DE SEQUENCES: 4

## (iv) FORME LISIBLE PAR ORDINATEUR:

- (A) TYPE DE SUPPORT: Floppy disk
- (B) ORDINATEUR: IBM PC compatible
- (C) SYSTEME D' EXPLOITATION: PC-DOS/MS-DOS
- (D) LOGICIEL: PatentIn Release #1.0, Version #1.25 (OEB)

## (2) INFORMATION POUR LA SEQ ID NO: 1:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 3018 paires de bases
- (B) TYPE: acide nucléique
- (C) NOMBRE DE BRINS: double
- (D) CONFIGURATION: linéaire

## (ii) TYPE DE MOLECULE: ADN (génomique)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 1:

TGATAGGTGC TTGTAAACTG TGCTAACGAA AACACATACCG TGTGCTGTAG GGACTTAAC	60
CTTGTAACTA TCAGTTAGCC TGGTTTCGCT AACAGTACAT CATTGGCTT AAAGTCACAG	120
CTTACGAGAA CCTATCGATG ATGTTAAGTG AGGATTTCT CTGCTCAGGT GCACCTTTTT	180
TTTTTTTAA GACGGAGTCT CTTCTGTCA CCTGGGCTGG AGTGCAGTGG CGTGATCTGG	240
GTTCACAAACA ACCTCTGCCT CCTGGGTTCA AGCAATTCTT CTGTCAGC CTCCCAAGTA	300
GCTGGGATTA CAGGCACCCG CCGCCACACC CGGCTTATTG TTGTATTTT AGTAGAGACA	360
GGGTTTCACT ATTGTTGACC ATGCTGGTCT CGAACTCGTG ACCTCATGTG ATCCACCCGC	420
CTCGGCCTCC CAAAGTGCAG AGATTAGAGA CGTGAGCCAC ATGGCCAGC AGGACCACTT	480

FIG 8A/1

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TTTACGAGAT TCAGTCCCAG TGTTCATTTT CTGGATGGGG AGAGACAAGA GGTCCAAGGT	540
CAAGTGTGCA GGTAGAGACA GGGATTTCT CAAATGAGGA CTCTGCTGAG TAGCATTTC	600
CATCCAGACA TTTCCAATGA GCGCTGACCC AAGAACATTC TAAAAAGATA CCAAATCTAA	660
CATTGAATAA TGTTCTGATA TCCTAAAATT TTAGGACTAA AAATCATGTT CTCTAAAATT	720
CACAGAATAT TTTTGTAGAA TTCAGTACCT CCCGTTCACCC CTAACTAGCT TTTTGCAAT	780
ATTGTTTCC ATTCAATTGA TGGGCAGTAG TTGGGTGGTC TGTATAACTG CCTACTCAAT	840
AACATGTCAG CAGTTCTCAG CTTCTTCCA GTGTTCACCT TACTCAGATA CTCCCCTTTC	900
ATTTTCTGTC AACACCAGCA CTTCATGTCA ACAGAAATGT CCCTAGCCAG GTTCTCTCTC	960
TACCATGCAG TCTCTCTTGC TCTCATACTC ACAGTGTTC TTCACATCTA TTTTAGTTT	1020
TCCTGGCTCA AGCATCTCA GGCCACTGAA ACACAACCC CACTCTCTT CTCTCTCCCT	1080
CTGGCATGCA TGCTGCTGGT AGGAGACCCC CAAGTCAACA TTGCTTCAGA AATCCTTCTAG	1140
CACTCATTTC TCAGGAGAAC TTATGGCTTC AGAATCACAG CTCGGTTTTT AAGATGGACA	1200
TAACCTGTCC GACCTCTGA TGGGCTTCA ACTTTGAAC GGATGTGGAC ACTTTCTCT	1260
CAGATGACAG AATTACTCCA ACTTCCCCCT TGCAAGTTGCT TCCTTCCCT GAAGGTAGCT	1320
GTATCTTATT TTCTTTAAAA AGCTTTTCT TCCAAAGCCA CTTGCCATGC CGACCGTCAT	1380
TAGGGCATCT GTGGCTCAA GGACAGCGGC TGAGCCCCGG TCCCCAGGGC CAGTTCCCTCA	1440
CCCCGGCCAG AGCAAGGCCA CTGAGGCTGG GGGTGGAAAC CCAAGTGGCA TCTATTCAAGC	1500
CATCATCAGC CGCAATTTC CTATTATCGG AGTGAAGAG AAGACATTG AGCAACTTCA	1560
CAAGAAATGT CTAGAAAAGA AAGTTCTTA TGTGGACCCCT GAGTTCCCAC CGGATGAGAC	1620
CTCTCTCTT TATAGCCAGA AGTTCCCCAT CCAGTTCGTC TGCAAGAGAC TCCGGTGAGT	1680
AGCTTCTGCG TTGCTGGCTG GGTTTCCCCC CCACGGAGGA GTCTCTCAC TCAGCACCTC	1740
CGGCAGCTCA GCTGTGCACA TGGGCACTGG GGGAAAGGATC CTGGCAGCAG CTCTGCTGG	1800
CTCTGTCTT AAGTGTGAAG CAGGGAGGAG AGGAACAGGT CTCAGATATT TCACCAAATC	1860
TCAGCAAAAT CCAGAGGGAG ACCGCAGGAG GTGGGGTGAT TCTTATGCTC TGGCTTTTC	1920
TCTCTGAAAA AAAAAAAAATCTTGCTTT TTATAAAAGT GGGTGGAACT CAGTTAATT	1980
CATCCTGTAA AAATAAATAT TCCTTCTCA GAACAAATTC CACACAGCCC AGATGTACCT	2040
GTTCGTTTA ATATTATTCA TCTTGGTAAG ATTATTCAG TTTCTCTGGC TAAAATCATG	2100

FIG 8A/2

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ATGTTATTCT TCTTTAATT ACCAATGGCC ATTCTTCTG AAACACAGAA ACCCTAGAAA	2160
GAGAACAGTC ATAGGCAAGG AATTTTTTC ATGCATAAAA TGTTGGGTT AAAGAGAGAG	2220
AGACCTAGCA ATCGCTTGG TCCACCTACC TCACCTCATA AGTGAGGAGT CAAGGCACAC	2280
TAGAGTGAAA TATATCTAGT GGGCACATGA CAGAGCCGG ATTAAAACCTT TGTTTAGGA	2340
AACTCTCCC A GCCTCTGGGT TTCATTTACA GTGATGCCA GGAGGGAAAT CACATTCCCC	2400
TGGCTCACCT CTCTGATCAT CCCTCCAGTG TGACTCTTGT TCTTAATTCG AGAAATATTT	2460
ATTGAGCATIC TACTAGTGCC AGCACTGGC AAGCAACTGG GGGGACAGCA GTGAGTAAGA	2520
AAGACCAAAA TTCCAGCTGT CTTGGAACCT AGGGTCTGA AGGGAAGATG GGCATTGAAC	2580
AAGAGTGACA TTGTCAGGAG ACGATGTTCT GGGTGCCACA GGATCATGTG GCAAGGAGAG	2640
CTAACCTGGT CCAGGGAGAC AAACCCCTCTC TGAGGAAATG ATGACAAGCT GAGACCCAAT	2700
ACTATTGATT AGCCATGGTT TTCTTAACC TAAGGTGGC CAGGCATGGT GGCTCATGCC	2760
TATAAACCCA GCATTTGGA AGGCCAGGC TGGAGGATTG CTTGAGCCCA AGAGTTAGAG	2820
ACCAGCCTGG GCAACAGGGT GAAAACCTAT CTCTTTGTA CTAAAAATTC AAAAATTAT	2880
CCAGGCATGG TGGCACATGC CTGTGGTCCT AGCTACTCAG AGGCTGAGGT GGGAAAGATCA	2940
CTTGAACTCG GGGAGTTGA GGCAGCAGTG AGCCGAGATC ATGCCACTGC ACTCCAGGCT	3000
GGGTGACAGG AGTGAGAC	3018

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## (2) INFORMATION POUR LA SEQ ID NO: 2:

- (i) CARACTERISTIQUES DE LA SEQUENCE:
  - (A) LONGUEUR: 11451 paires de bases
  - (B) TYPE: acide nucléique
  - (C) NOMBRE DE BRINS: double
  - (D) CONFIGURATION: linéaire
- (ii) TYPE DE MOLECULE: ADN (génomique)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 2:

GATCCACCCG CCTTGGCCTC CCAAAGTGCT GAGATTACAG GTGTGAGCCA CCACGGCCAG	60
CCGACACTGC CCTAACTCTC AAGTTGCATC CTTACTCGAA TAGTATGACA GTGTGGGAAG	120
CAGCATGGGA CAATGTAAAA AGGAGGCATG TTTCTGGCTT CTGCTACTTA CTAGCTGTGT	180
GTCTTGCAC GAGTTCTTA ACCTCTCTGG GCCTCAGTTT CCTTATCTGA AAAATAACAA	240
TGATAGTATT CCCTTCACAG GCCAAATGG AATACTATCA CGAACACTAC ATAATGGAAC	300
TCAATAAATA ATAGCTACTG CGGCCGGGCG CGGTGGCTCA CATCTGTAAT CCCAGCACTT	360
TGGGAGGCCG AGCGGGGTGG ATCACAAGGT CAAGAGATGG AGACCACCT GCCCAACATG	420
GTGAAACCGT ATCTCTACTA AAGATACAAA AATTAGCTGG GCATGGTGGC GCATGCCTAT	480
AGTCCCAGCT ACTCGAGAGG CTGAGGCAGG AGAACACTT GAACCCCGGA GGCAGAGGTT	540
TCAGTGAGCC AAGATTGCAC CAGTGCACTG CAGCCTGGCG ACAGAGTGAG ACTCCGTCTC	600
AAAAAAATAC CTATCTATCT ATCTGTCTAT CTACTGTTAT TCTTACCTGG TCATTTCTT	660
TTTGTTCAC AGGAAATTG CGAGAATCCC CGATTTATCA TTGATGGAGC CAACAGAACT	720
GACATCTGTC AAGGAGAGCT AGGTAGGAAA GTGCCTCAGG TCAGATCCTG CCAGATGATC	780
AAGGGGTGAT TACAAGGTGT GATCCCTTC CAGGAGGTAAGGGACAATC TGTGCTTGCT	840
TCCAGTAACT TTTGGAAGA TTTTTATAA CAGTTGCTTT ATGGTCGTTT ATCTACATGC	900
TGGCGATTGC TTCACTTCCT CCTACATGCC TCTTAGCAC TCTGCCATGC ATCACAGGG	960
GTATCTGCAT CCTGTGGCCT CCTCTCCAGT ATCTCAAGGA CACTTACATA CCCCCACTCAG	1020
CATGACAAAA GCCCTGCTTT TCACTGTATC GTCTTCTTG GAAGACAGCT CTGTGACTGT	1080
GCACCAAGCA TGCCCCTTGG GCATGGAGAT TCTAGATACA CACACAAAAG GCATGCCAA	1140
GGAAAGCACT TGTAACTGGA ACCCTTGGTT TAAATTGGCC CAGCATAGCT CCATCTTAA	1200

FIG. 8/B1

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AAGACTCTT	CCACAAAGAT	GGCATCCGCC	ATGTGGATGA	GCATCCAATT	TTCTCTTGAA	1260
TTGGTTAGCT	TGACTGCTCC	ATCTGATCTT	CCTCTCTCTC	GACCTCTTGT	TCAGAAAGTA	1320
TTGTCTTGG	TGTGGACTAT	AAGCAAGCTC	TGTGAAGTAA	AATTGGAGAG	AACACCAACA	1380
GAAACAATTT	AAATTTGAGG	AAAAGGGGGC	ACCTAAGACC	AAAGGAATT	GGCTTATTTC	1440
ATTCCAGAAG	GGGAGGCTGA	GAATAAATCA	GATGAATATC	TGGGTTCCCTG	CACCTGAGGG	1500
AAGGCTTCCT	GCAGAGCCCT	GGGCATAATA	ATCTGGGACC	TTCAAACCAA	TAACCTCTTT	1560
TCCAAGGAAA	GAETGGCTGC	TTCCAAGGAG	GGTAGGGGAG	AGTCGGGCTG	CAGGCAGCTC	1620
TCAAGTCTCC	CCTTGCACAC	TCTCAGGTTG	GCATTTTAC	TTAACCCAT	CCTCCCTTAA	1680
GAAGGCAGTT	CTTTGTGACC	AGGGTACACC	CCCTATTATA	TATATATATA	CACACACAGA	1740
GAGAGAGAGA	GAGAGAGAGA	GAGAGAAAGA	GAGCAAAGTG	TTACCTCCAA	CTACATACAG	1800
TACTCTGTCA	GAAAAGAGGT	TCAGAGAATA	AGAAAACGTC	CCGAGCTCAT	TCCGTTGCCA	1860
GCAATGTCTT	ACTGCCCCCT	ATAGACGGGT	TCCAGGGCAG	CTGCCTACCT	GGCCTTCCTT	1920
CCAATACAAA	TCATCTTGGT	GGATGGTTCT	CTGAGGCTCA	GTCTTCGCTG	AAGTCAGAAG	1980
AGGAATTGGA	CTCACATTGC	AAAGGCACAG	GGCAGGGCAG	ATTCCTACA	GGTGTAGGA	2040
AGAACAAACCC	AGTTATGATC	ACCTACTGCT	CTGTCTCCAT	TGAGGCCTAA	AAAGGAAGTG	2100
AGTTTATACT	GCAGTTGGAG	GAAC TGCTG	CAGCCTTGAG	GAAAATGTCT	AGTCACAAGG	2160
GAGTAAGTTA	CCTGTTGATC	ATATTGTCAA	GGAATTCCCTG	TCCAATTCTC	CTTCCCTGGG	2220
TTGACACCTC	TGTAAGGTCA	GATCTGGAAG	TAGGAGAGTG	GGCACCAAGG	GAGTCCCCGT	2280
TCAGGGAAAGT	GGAGTGGCTG	GCTGGGATTG	GGGCTTTTTC	TTCCCAGGAG	GAGCAGGAGT	2340
GCTCACGATC	TGTGCCCTGT	GTCTGCCCTGC	AGGGGACTGC	TGGTTTCTCG	CAGCCATTGC	2400
CTGCCTGACC	CTGAACCAGC	ACCTTCTTTT	CCGAGTCATA	CCCCATGATC	AAAGTTTCAT	2460
CGAAAACATAC	GCAGGGATCT	TCCACTTCCA	GGTGAGGTAA	TGAGAGTGT	GTAAAGAGGG	2520
CCAGCGGCAG	GCCACCCACC	GCTGGCTC	TGGCCTTGAC	TTCCCAGAAG	CTGGAGGAAA	2580
CTTCCCACCC	ATCTACCCGC	AGCGGCAACA	GTGGCATGG	ACCCCCCTAA	GGCTTCAAGC	2640
CTGGGAGGAA	GCAGTTGCTT	ATCTCTGGCT	CCCTAATCCC	TCCCCCACCA	CCTTCCACTA	2700
TGTCCCAGAA	AGACAGGAAG	ACATCCTGTT	TACTGTGGGT	CTATTTTGT	CTTCCAGCT	2760
GTCTGGCTGC	TTTATTGCC	TGCAGCCCTT	CTCAAGTAGG	TCCCTAAGAT	ATTAGCACTG	2820

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TGACACCACA GGACCCCTCA GGTTGTACAG GAACCCCTGT CCAGGGCTCC TGTATACTTC	2880
TTCCCTCTCTA AGGCATGGCG GTACCAAGGC TATCACTCCT CTCTTCCAAG CCCTGGAAGA	2940
AGAGTCTGCT TAACCTGGGG ATCAGGCTTC TTGTTTGCCT TAGAACTGAA TCTGATGGTT	3000
CTAGAATCCA TCCAGCTACT GGAAATTTC TGGGTCCCAG TCACCTTGGC ATAGAGCTGG	3060
TGCTAGAGCA GAACCAAACG GAATTCTACC TGTGAGGGTC TCGTAGCTTC CGGGATGCTG	3120
GGGAGTCAGC CTGCTCCAG CTTCAAAGGC TCCCTCATGT CCCAGGATGA CCCACATTAT	3180
CAGTTCTTGC TCCCCGGGTC TTGCACCTCA GCACCGAAGG CCTCAGAAAA GGTCTGTCTC	3240
CAGGCTCAGA CTCCCCCTCC TGCCGCCCTG GGAACATGGC ATATTAAAG GGTCTCAGAT	3300
CTAAAGGGCC TTACATACAA ATATCAGATA GATTCTGTT CTCATTTCAA TGAGGGAGAA	3360
AGTGCCATTG AAAAGGAGAC TAAACCACAT TTGGCCCTT TCAGTTCAA CTGATTCAATT	3420
CAAAAAAGAG CGACATCCAA ACTTGAAATG ATTGAACAAT GTTCTGCTA CAGCTAGAAT	3480
AGATTCTGGG TCACTTTGTT CCTCCGTTTC AATCCTTGTGTT CTTCAGTTG GCATCAAGAA	3540
ATACCTAAAT CAGCACAGTG CCTTCACTGC ATAGTTCCA ATCCTGGCCA CATTGAATCA	3600
GCTGGGGGCA CCTGAGACTG CTGACACCCA GGCCCTGCC CAGACCTGCT GAGCAGGAGA	3660
ATGAAAATCT TACATCCTAA GACACTCATG GAGCACCTAC TCTACCCATT ACTGGGCTGG	3720
ACTCTGTGGA AGACATGAAG TATATGTAAC TCACTTCCAG CTCTAAAAA GCACCCAGTC	3780
CAGTTAGAGA CAGATTACA CACCCAAAC ACAAAATAGG ATGAACAGGC ACCCAGATGC	3840
AGAGTCCAGG AAATGATGCT GCTTGGGAT TCAAGAACCC CCTGAGGAAT GTGGAGGAAG	3900
GACACATTTC CTAACAGTAA TTGAGTATG TGACTCTGTC CGTGACGGCTT CTGTGCAGTT	3960
CTGGCGCTAT GGAGAGTGGG TGGACGTGGT TATAGATGAC TGCCTGCCAA CGTACAACAA	4020
TCAACTGGTT TTCACCAAGT CCAACCACCG CAATGAGTTC TGGAGTGCTC TGCTGGAGAA	4080
GGCTTATGCT AAGTAAGCAA CACTTTAGAA TGTGAGGTGG GGCTAGAGGT GAGAAACTGG	4140
GTTGCAAAT CCAGCCGAGA CCTCACTCAC AGGAAGAGGC ATGTGCCTCT ATACGTGCAT	4200
ATGTGTGGGC ATGCAAGTCC AACTGTGACC CAAAGTTAGA GATCAGTTCC AGGCAACAAAC	4260
AGCTCTAACT AAAAACATTA AATTAAAGAG TAGAAATGAA GATTGCTATA GAAGACCTTT	4320
AGCTTTAGCT CACCATAGCG AGTTCTTCA TTGCACCTCC ATGGTGGCAT TGCAAGTCTT	4380
GGGATCAGAG CATTGCTCCA GGGTCTCGAT TGGCTCAACC TCATGTGCTT ATAGAAGATT	4440

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TATAAAGACA TGTGTCCTCT CAACTAAAA GCTCCACCCC AGATGATAAT AATGGATTTT	4500
CAAATTTGG ACAAGGTCA CTCTGTAATG CAGGCTGGAG TGCAGTGGTG CAGTCACGGA	4560
TCACTGTAGA TTGACCTCCT GGGTTCAAGG TGCTCCTCCC ACCTCAGCCT CCCAAGTAGC	4620
TGGGACTACA TGCGGGCATC ACCATGGCCC TTTTATTTT GTATTTTTT GTAGAGCGGG	4680
GTTTCCCCT GTTGACCCAG ACTGTTCTCG AACTCTGGG CTCATACAAT CCACCAGCCT	4740
TGCCCTCCCC AAGCGCTGGG ATTGCCGGTG TGAGCCACCA CACCGGCAGC TGCTAATGCC	4800
TTTAATGCAG CCCTTCCTCA ACGTTCAGGA TGTAGTGGAA AGAGCTCTCA GGAAGTGGGG	4860
ATAGCTGGGT TTCAATCCCA GTGCTTCTGG CTCTCTGTGG TCTTGGGTGG GTCACTTAGC	4920
CTCTTGAGCT CAGTTCTTC ATTATGAAGA AACGGAATCA TTGTTTCCAT CCCATGAGCT	4980
CATAGGGTTA ATGTGGAATT GATGAAAGAA CATCACAGCA TCCAAGAGGT AAAGTTCTGG	5040
TGGCAGTGGT ACCTGGGTTT TGTTCCCTGG AACTCTGTGA CCCCAAATTG GTCTTCATCC	5100
TCTCTCTAAG GCTCCATGGT TCCTACGAAG CTCTGAAAGG TGGAACACCC ACAGAGGCCA	5160
TGGAGGACTT CACAGGAGGG GTGGCAGAGT TTTTGAGAT CAGGGATGCT CCTAGTGACA	5220
TGTACAAGAT CATGAAGAAA GCCATCGAGA GAGGCTCCCT CATGGCTGCC TCCATTGATG	5280
TAAGTCTGGG GTGTGGGGCA CAGGGTGGGG AGCTCCAAGT GTCAGGAAGC CTTTTACCCA	5340
ATGAAGGGCA GCATAGAGCT TTTGTGTGGG ACAGAGCGAA TGTTTGTGG GAGGAAGCAG	5400
GAACCTGGCTC TCAACTTTGA GGACTGGAA TTTCTCAAGG GAGAACAGTT CTTCCGGATT	5460
TTCAATAAAG ACACTGGTCA AGGACATTTC AAGCCCTGGA ATGTCAGTGG AAATCAGTCC	5520
AGAGGCCTGT GTCAGTGGAG GCCTCCCTTG CTGGTGCTCC TCAGTCTCAG CACGCTCCCA	5580
TTAACGCTGGC CACGTACTTG GCTGTGGACC TGAGCCCACC ATTTCCCTAA GAAAGCCTCC	5640
CAGTCACTGG GCTTTCACCA CACCTCCCCG CTTGAGACGT GGGCTTGTG TTGTTACCTG	5700
GGAGAAGCTA AGCCTGCAGC ACCTTTCAGT GCAAAGAAAT GCTGTGAACG GAGACAGGAG	5760
CCAAGGGTAG GGAGATGGCC GCCCATGGCC AGGCCTCCTT CAGGGGGCAT GCCTTCCCTG	5820
AGGGCTGCTC AGTATATTGA TATGATAATC TTAGTGGTTT CCATTGGGA GGATGGGCT	5880
GAAGCTGAAT TCCTGCCCC TCTTCTCCCA ACACGCCAA TGGACAGCTT GGAAGGTCA	5940
TTAGCACACA ACACCATGGA TGAACCTTTT TTCTGTATCA CTTTTCTCCG TCTTTCTCC	6000
ATTCTGTGCTC TGTTGATCTC TCCTCTCTCC CTTTGTCTGT CCCATCTCTT TCTCCTCTCT	6060

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CCTTCCCTTT CCACCCCTCT GTGTTGTC TCTCCCTCCC CTGTGTTGTT CCCTACATTC	6120
TCCATCGGGC CTCAGGATGG CACGAACATG ACCTATGGAA CCTCTCCTTC TGCTCTGAAC	6180
ATGGGGGAGT TGATTGCACG GATGGTAAGG AATATGGATA ACTCACTGCT CCAGGACTCA	6240
GACCTCGACC CCAGAGGCTC AGATGAAAGA CCGACCCGGG TGTGTACACC TCCGATTATC	6300
AGAACTGACC ATCCCTCCAA CCCACATGAC CCCGCCCTAT TAGTGTAGA CTCCCTCAG	6360
CAGCCAGGGC CTTACCCACA CACCCCCACC TGGCACCTCC CAAGGGTCTG GGTTGAAATA	6420
ACTTGCTCAG CCAAGGCTCC TGAAGAGGGT GCAAGAACCA GGATTTGGA GGGAACTCT	6480
GCTGGAGTTT CTGCATATT CATGGTCCAG GCAGTTCCCTC TCATAACGAA CTATCAGACA	6540
GAAATACTTG TAAAGATACT TCATTTATTT TGAAATATTT TTCCCTCTCT AATGTATTCA	6600
TTTATTCACTT CAACACTTAT TTTTGAGCTC CTACTATGTT CCAGGCACTC CTCTAGCAA	6660
CAAAGCAAAT TCTCTCCTCT TTTTCAATAT TTGTGGAAAA AGCAAGGTCT CCCTCTTGTA	6720
GAGTTTATAT TCTAGTATTTC TCATAAGTTA TACCTGCTCA CTGGAGAATA CTGAGCCATA	6780
CAGAAAAACA CAGAGGAAAA TTTCACTTAT ATTTTCCCC ATGTAAAGAT AACCACTCTT	6840
AACATCTAGT ATATGTTCTT CCAGGATTTT TCTATGCACA CACTGAATCT GTATTTTAT	6900
TTTTAAAATG TTATCATATT GTATGTACCT CTTTGCAGCC TGCTTTTTC AGTTAGTTT	6960
TTTGGTTTTT TGGTTTTTTT TTTTTTTGG AAACCAAGTC TTGCTCTATT CCCTAGGCTG	7020
GAGCACAGTT GTGCCATCT CGGCTCACTG CAACCTCTGC CTCCAAAGTT AAACTAATT	7080
TCCTGCCTCA GCCTCCCGAC ATAGCTGGGA TTACAGGCAC ACACCACAC ACATGGCTAA	7140
TTTTGTATT TTTTAGTACA GACGGGGTTT CACCATGTTG GCTGGAATGG TCTTGAACTC	7200
CTGACCTCAA GTGATCCACC TGCCTCAGCC TCCCAAAGTG CTGGGATTAC AAGTGTAAAGC	7260
CACCAACACCC GCCCTAGTTT GATATTCTTA ATGTGCCAA AGTATTCTCC TGTAACTTT	7320
TTTAATAGCT ACACAATATT CAAACACACA GATATGTTAT AATTTATTTA CCCAATACCC	7380
TATTATTGGA AAGTTGAGTT CTTTTTTTC TTGTTTTGT TTGTTTTGC TACTATTCTA	7440
AAATGCTATA ACGAACATCC CAATAGATAAC ATCTTGTAT ACATCCATGG TGACTTCCAT	7500
AGGACAGATT CCCAGCAGTA GAATTGCTGG GTTGAATGAT ATGCTTAGGG TAATGACAGA	7560
AGAGTCATT CAACCAGCTT CCTAGGGTCT TAGAACTTAA GGATTAATGA GTCTTCCCGC	7620
CCCCCTCCAG TCTATTCAAGC ATGATCTGGA TCATGAGGAC TGAGATCTGG AAGAGACTGA	7680

FIG. 8B/5

SUBSTITUTE SHEET (RULE 26)

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GATCTGGGAG AGGCTGAGAT ACCAAAAGCC CTGGCTCCAC CCATAACCCCT CGCCCTGAAA	7740
ACAGCTCTAG GAATTCCCGG GCCTAGCAAG GCTCCGGGAA GCTCCTTTA AAGCTGTGAC	7800
GTTAGTAGGC ACATGGACCA TAGAGACCTA TCCAGGGCTC ATGGGACTTT AGTGATCCTG	7860
CCCTTCTCCC AAGGATCCCC CATGGCTGCA ACTTGGAAAT TTCTGCAAAT GGAAGAGCTA	7920
CTCCTTAGGC ACGGTCAATGT CTGAGCAGGG ATCTCCTCGG GCTTCTTAG AATTCTCTCC	7980
CTGGGCACTG GGACTCTTGA TTTCTTGAAT ATTATGTTCC AGGTGGGTGT GGAGGAGGTG	8040
AGGGGATGTA AAGAAGGCTA GACTTGGCCA GCCGCAGTGG CTCATGCCTG TAATCCCAGC	8100
ACTTTGGGAG GCTGAGGCCG GTGGATCACC TGAGGTCAAG AGTTGGAGAC CAGCCTGGCT	8160
AACATGGTGA AACCCCGTTT CTACTAAAAA TACAAAAAAAT TAGCTGAGCA TGGTGGCACG	8220
TGCCTGTAAT CCCAGCTACT CGGGAGGCTG AGGCAGGAGT ATCGCTGGAA CACGGGAGGC	8280
AGAGATTGCA GTGACCCGAG ATCGCCACAC TGCACCTCAG CCTGGCGAC ACAGCAAGAC	8340
TCTGTCTCAA AAAACAAAAA AGAAAGAAAA AAAGGAAAAG CTAAGACTTA CATGTGTAC	8400
TTAACCCCTT TTCTCAAACC TCTTCTCTT CCAGGAATAG TCAACCCCTG GATGGCTTCA	8460
GGGGAAGGGG GATCCTGAAG CCCAGGGCAG CCTCCAACTC TACCCCTTCC TCCTTGAAG	8520
GATACTAAGG CGTCCAGAAA GGAGGGGCAG GACACTGTTA CCCACCCAC ATCCCAGCAT	8580
CCACATTGCT CTCTGATGGT CAGGACAGAG CCTTCTCAGG GAGACCAGCC TGTCTGGAGC	8640
TGTGTCTCTT GGCACCTTA AAGGGCCACT GAAGGTCCGT TCGTGGTCGT GAGGCACACT	8700
TTCAGGGAGC AGAGTGGTCT GTGTCTTCAC AGAGCCCGGA AAATGAACTA GTATGAACCT	8760
TGCCTCCAAG CAGCAGAACT TCTGTTCCCC CGCCCCTAAT GGGTTCTCTG GTTACTGCTC	8820
TACAGACAAT CATTCCGGTT CAGTATGAGA CAAGAATGGC CTGCGGGCTG GTCAGAGGTC	8880
ACGCCTACTC TGTACGGGG CTGGATGAGG TAAGCCTGGT GGGGCTTGGT GGGGCAAGGG	8940
CACCCCTCTG GGTTAACCTC ATGAAGTCAG GACTTAGCTG TTGGGGCCCC TGCCTCTCT	9000
GGAGAGCTTG CCTCCAATCA GGACATTCAAG TTCAAGGTCC AAGCCACGCC TGGGAGCAGA	9060
GGGGCCTGTG AAACTGGTAG AGGTGGATCC TCCCACAGTT GGTGCACAGT TTATCTTGC	9120
TTTCGTGCT AAAGATGGCA ATTTTCCAA CATTCCAAT GAACAAATTG AAATATCACT	9180
TAACCTTGCT TTTACAAAGT TGGTTTCATG TGTTCTTGAG CTTCCGTTC TCTCGTGTTC	9240
AGATAGCTAC AGTTGTCTCT GGGTAGCCAC GGGGACTGGT TCCAGAAGCC CCAACAGTAA	9300

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CAAAATCTGC AGATGCTCAA GTCCCTCTG TAAAATGGAG TACTATTGC ATATAACCTA	9360
TGCACATCCT CCCATATACT TTAAGTCATC TCTGGATTAC TTACGATACC TAACACAATG	9420
GAAATGCTAT GTAAATAGTT ATTGCACTGC ATTGGTTTT TTTGGTATTA TTTCTGTTG	9480
TTGTATTATT ATTTTTCTT TTTTGATAA TTTTGATCC ACAATTGGTT ATATGCCAAA	9540
GCCATGGATA CGAGAGGCTG ACTGTTCTGT TTTGCTCCTT CTGGGACTTC TGGGTTTCC	9600
TGGACCATGT CTGAGACAGG AACGGTGTAA GACCTGTTGC ACACAGTTGG GCAGGTTGTG	9660
CCCTGTACAG AGGGATGGGC TGAGAGGGC AGTTGCCTGC ATCACCCATT GCAGCAGACT	9720
GGAGGGAGTC TGCTTGTIG TAGTCCTCA GTCAGCAGGG GCCTTTGTG TTTCTTCCT	9780
TTCCTTTTTT TTTTTTTTG AGACGGAGTC TCACTCTGTT GCCCAGGCTG GAGTGTAGTG	9840
GCACAGTCTC GGCTCACTGC AATGTCCGCC TCCTGGATTC AAGCGATTT CCTGCCTCAG	9900
CCTCCTGAGT AGCTGGGATT ACAGGCGGT GTCACCATGC CCAGCTAATT TTTGTATTT	9960
TAGTAGAGAT GGGGGTTCT CCATGTTGAT CAGGCTGGTC TCGAACTCCT GACCTCGTGA	10020
TCCGCCACC TCGGCCTCTC AAAGTGTGG GATTACAGGC GTGAGGCCACC ACGCCTGGCC	10080
AGCAGGGCC TTTTTCTAA TTTATATGAA GACACCTAAT TTATATGTGT TAGCAAAGCC	10140
CTCCTGTTA TGCCCTCACCT CCTCCCCGA AGCTCATACG GCAGGATGTT CCTGAGAAAA	10200
TTGCCTCTTA GAAGATAGAG AGGAGATGCC AAGCCTAAGT TAGGCAGACT CAGGAGGATA	10260
GGTCTGACCC ACCCCCCTGCC ATTCCCCAGC ACACTTGTGA TTAATCTCCT TGGCCAGAGC	10320
CAGGCAGAAC ACCCTCGCGT AAGAGATTTG CCCCCCAGCC CCGTCCCAGC CCTCAGCTAG	10380
ACAGAAGATT CCCTTTCCAG AGAGGCTGCA GACCATGAGA GCTCTTCTG TGTGCTTAAG	10440
GTCCCGTTCA AAGGTGAGAA AGTGAAGCTG GTGCGGCTGC GGAATCCGTG GGGCCAGGTG	10500
GAGTGGAACG GTTCTTGGAG TGATAGGTAG GTGAGGGAC CCCACGGGAT TGGCGGTGGC	10560
GGGGAACAGG GTCCGGGACA AGGCTGTGTT GGGAACTGAG CCATGAGAGT ATTGAAGATG	10620
CTTGGTATAA AATCACCCCTC AAAACCAATG ATCCGCAGAG AAGAGGGCA CAGGTGTTGG	10680
CTCCAGGGAA GGGCCAGGAG TGGAAACGGG GTGCTGGGA CCCAGAGAGG TTGCTGACAA	10740
CCATTGGCTG GAAAGGAAGG ATTCCAGAAA GCGTGGGAA GGTCCAGGCA GGAAAAGCGT	10800
ATGAATGCAG GTTCTGGGC TAGAGAAGTG ACTTCCCTTC TTGGGGTCTT GTGTTGCCTT	10860
TCCTGTGAAA TGGGAACAGT ATTATTAGCA CTTACCTTGT GGGCTGATAT TGAGGAGTAA	10920

FIG.8B/7

SUBSTITUTE SHEET (RULE 26)

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CTGGGACTTG TTTTGGGCA ACTGCTGAGC CATTGCTAAG ATTCCCCTTA CCCGTGCTTG	10980
TCCCTTGTAT TAAGGCACAA GGGCCCTTG AAAAGAATT TACCTGCTT ATCAATTGAA	11040
AGGGATTAAG ACCTTGGGG CCAACCCAAA ATAAACATGC GAACTTATTA TTTATAGGCT	11100
CCATGCACAC TTCGTAAAAC CTCCATGGTC CTACTGGTTC CTGATTACCT CCACTCAATG	11160
AGAGGCAATT CATTACTGAA TGAGCCATAA GCGCCTCTTA TTTGAGAGG GGGATGGCAG	11220
GACTCAGTCG AGGAGAAGGA CCGCACCCAG GCAGCCTGGG CCCCTGGCT CCTGTACTTA	11280
TTTACTGCTG GGTACTTCCT AGCCCAGCAT GTAATTACTG GTTCGTTCAAG TCATTGTTT	11340
AGTAAATGTT TCTTGGGCAC CTACTACATA GGAGGCACAG GTCAAGGCAC TGGGGATATT	11400
CTTTCTACCC ACCCCCTCCC TCCCTACACT GTGATTAGGG ACTGACCGAT C	11451

253350 \* FILED 25 SEP 1996

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## (2) INFORMATION POUR LA SEQ ID NO: 3:

(i) CARACTERISTIQUES DE LA SEQUENCE:  
 (A) LONGUEUR: 1834 paires de bases  
 (B) TYPE: acide nucléique  
 (C) NOMBRE DE BRINS: double  
 (D) CONFIGURATION: linéaire

(ii) TYPE DE MOLECULE: ADN (génomique)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 3:

ATTTTTTTTT TTTTTTTG ACGGGAGTCT CACTCTGCCA CCCAGGCTGG ACTGCAATGG	60
CGCGATCTTG GCTCACTGCA ACCTCCGCCT CCCGGGTTCA AGTGATTCTT CTGCCTTAGC	120
CTCCTGAGTA GCTGAGACTA TAGGTGCCCG CCACCACGCC CAGCTAATT TTGTATTTTT	180
ATTAGGACGG GGTTTCACCA TATTGCCAG GCTGGTCTCG AAATCCTGAC CTTGTGATCC	240
GCCCACCTCG GCCTCCAAA GTGCTGGAT TACAGGTGTG AGCCATTGCG AGCAGCCAG	300
AACTCAATT C TTAACCTTTA AAGTATGATG AGAAGAAGGA TCAAGCCCTC ACCAGCCAT	360
TTAAGGAGTT TAGGCTCACT CTTGAGGATG TGAGAACTCA TTGCTATTGG GTTTCACACT	420
GAGGTTAAC A GGTGAAGTCA GCATTTGGT AGTCACAGC ACCTGCAACT CTTTGTATT	480
CTCTGATAACC TCCTGTCCCA ACCTACATCA GGCTTCCCT TCTTCCTGCT TCCTTAATT	540
CTCCATTTC CCACCAAGATG GAAGGACTGG AGCTTGTGG ACAAAAGATGA GAAGGCCGT	600
CTGCAGCACC AGGTCACTGA GGATGGAGAG TTCTGGTGAG TCCAGAACCC AGGAAGACCC	660
AGAAGGGTAA GGGTGGGAA GAGAGGGAA ATCTCAGACC TCAGTCCCCA GCTAAGGTTA	720
TCAGATTCCA GCCCTTGGGA GATCTTGCT GTGTTCTCCT CCAGCCCAAG GCCCAGCAAG	780
GATGAGGTTTC TGAGAGGAGC CTTCCAGGCC ACAGGGACAA TGAGCCAGG ACCAGCCAA	840
CATGACATGG CTCTTGCCCTC CTGTGTGCC C TCCGCCACA CACTCTATT CAGCCACAGG	900
CACCCCTGGCC TTAGCACAAT TCTTTCTGA GCCTAGGAAG CTCCACTTAC CCTGATCTTC	960
CAACGTCAAC CTCACCCCTCT CTCAGGTTGT TTCTATTCA GCTTCAAGTC TCAGCTTAAG	1020
GAGAATTTC AAGTCTCAGC TTAAGGAGAG CCCCTAAAGT TCCCCGAGGA CTGGGATTAA	1080
TTTATGATGC TCATCACCCCT TAAAATTGTT TGCTTAAGCC GGGCGCGGTG GCTCACGCC	1140
GTAATCCAG CACTTGGGA GCCCGAGGTG AACGGATCAC GAGGTCAAGGA GATCGAGAAC	1200

FIG. 8C/1

SUBSTITUTE SHEET (RULE 26)

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ATCTGGCTA ACACGGTGAA ACCCTGTCTG TACTAAAAAT ACACAAAAAA AGTAGCCGGG	1260
CGTGGCAGCG TGCGCCTGTA GTCCTAGCTG CTGGGGAGGC TGAGGCAGGA GAATCACTTG	1320
AACCTGGGAG CCAGAGGTTA CAGTGAGCCC AGATTGCGCC ACTGCACTCC AGCCTGGCG	1380
ACAAGAGAGA CTCTGTCTTG GAAAAAAAATG TGCTTAGTTT AATGTCAAGG	1440
GAAAGGTTTT GGGTGTTTT ATTACTTTAT TTTTATTAA AAAACTATAA TAGAGACGGG	1500
CCTCGCTATA TTTCTCGGGC TGGTCTCAAA CTCCTGGCT CAAGCGGTCC TCCCACCTTG	1560
GCCTCCCCAA ATGCTGGCAT GTGGGCCTGG TCAACATATG GGACCCCAAC TCTACAAAAA	1620
ATTTTAAAAT TAGCCAGATG TGGTGGCGTG TGCCTGTAGT CCCAGCTACT TGGGAGGCTG	1680
AAGCAGGGGG TCACTTGAGC CCAGGAGGTT GAGGCTGCAG TGAACATATGA TTGTCGTTCA	1740
CTTTTCTTCT GAACGTGAGA TTAAGTGTAG TCACCAATTG GGCTTAGGAT TATTTATTCA	1800
GAATTTTAA CCGTCACGTT GCGGCAAACC AGGT	1834

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## (2) INFORMATION POUR LA SEQ ID NO: 4:

## (i) CARACTERISTIQUES DE LA SEQUENCE:

- (A) LONGUEUR: 14664 paires de bases
- (B) TYPE: acide nucléique
- (C) NOMBRE DE BRINS: double
- (D) CONFIGURATION: linéaire

## (ii) TYPE DE MOLECULE: ADN (génomique)

## (xi) DESCRIPTION DE LA SEQUENCE: SEQ ID NO: 4:

AGGAGGTGGA GGTTGCAGTG AGCCAAGATC ATGCCACTGC ACTCTAGCCT GGGCAACAGA	60
GCGAGACTCT GTCTCAAAAA ATACACACAC ACACACACAC ACACACACAC ACACACACAC	120
ACACACATAT ATATAACACAC ATATATATAC ACACACATAT ACACACACAC ACGTCTGTAT	180
ATATATGTGT GTGTGTATAT ATACACACAC ACACATTCT ATATATTCTT GTAGAGCTAT	240
GTGTGTCTCC TGTGCTATTG AGCATGAGCC CTTTTTTTTT TTTTTTTTT TTGAGACAGA	300
GTCTCACTTT GTCGCCAGG CTGGCATAACA ATGGCGCAAT ATCGGCTCAC TGCAACCTCC	360
GCCTCCTGGG TTCAAGTGAT TCTCCTGCCT CAGCCTCCCA AGTAACTAGG ATTACAAGTG	420
CCCGCCATAA TGCTCAGCTA ATTTTGTAT TTTCAGTAGA GATGGGGTTT CACCATGTTG	480
GCCAAGCTGG TCTCAAACTC CTAGCCTCAG GTGATCCACC TGCCTCAGCC TCCCAAAGTG	540
CTGGGATTAC AGGCATGAGC CACAGCACCC TGGTGAGCAC TAGAGCTTAT TTCTTCTATC	600
TAACTGTATT TTTGTATCCA TTAGCCACCC TCTTTCATC CTCCCCCTCTC CTTCCCTTCC	660
CAGCCTCTGG TAACCACTGT CTGCTCTCTA CTTCCATGAC ATATGCTTTG TTTTAGCTCT	720
CACATATGAG TGAGAGCATG CGACATTAT CTTCTGGCC CTGGCACATT TTTGAATCAT	780
TGTTAGAAAA GATGATGGTT TGGAGTAGAT ACATCAGAAG TGACAGCGTT TGCCCTAAAA	840
AGGAAAGACA GGCTCCTCTG GGACCCCTGAC CAAGTTCCCTG TGAACATTATT TATTATTGTG	900
CTGTGTTAGT CCTGGGGTCT TCCGTTCCCA GCCCTCCTCA CCTGCTCCCA TATGGCTCTC	960
TCTCTTCTTC CAACCTCTCA GGATGTCCTA TGAGGATTTC ATCTACCATT TCACAAAGTT	1020
GGAGATCTGC AACCTCACGG CCGATGCTCT GCAGTCTGAC AAGCTTCAGA CCTGGACAGT	1080
CTCTGTGAAC GAGGGCCGCT GGGTACGGGG TTGCTCTGCC GGAGGCTGCC GCAACTTCCC	1140
AGGTGGGAGA TGCTCTTGAT GGGGGGAGGG TCTAAGCCGA AAAAGTTCCA GCCAGAAGAA	1200

FIG. 8D / I

SUBSTITUTE SHEET (RULE 26)

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GCCTAACTAG TGCTTATTAA GTCTCTGT TCCAGACGTC CACTATCTTA TTAAACCTTC	1260
CCTGTTTAC TGAGAAGGAA ACCACCATGC TGAGAAGTTT GCAATAGGGA GCTGGTAGC	1320
AACTTTGGAA GCAGGAACCTT GTGGGAACAA TGCAGATGCT GCTTGGACTT ACGATGAGGT	1380
TATGTCCAGA TAAGCCCATC CATCTTTGA AAATACCCCTA AGTAAAAGT GCATCCAATA	1440
TGCCTAACCC CCCAACCTC ATAGCTTACC CTGGCCTACC CTCAAACATT GCTCGGAACC	1500
CTTGACCTTA AGCCTAAAGT TGGGCCAAAT CATCTAACTC CAAAGCCTAT TTTACAAAGA	1560
AAGTTGTTGT AATATCTCCA TGTAACCTAC TTAATACCTG TACCTAAAAA GTGAAAAACA	1620
AGAATGGTTG TACGGGTACT CGAAATCCAG TTTCTACTGA ATGTGCATCT CTTTCACATT	1680
GTAAAGTTAA AAAATTGTAG CCGAACCATC CTAAGTCAGG GACTGTGAGT ACTGTGTCAG	1740
TAACAGTAAG GGCACTATTG GAGAACCAAG TTAGCAGCTG CTGCAATACT TCAAGTCAGA	1800
GATGATGAAA ACCTAGACCA AGTCAGTAGC AGCAGAGATG GAGGGGAGAC AGCAGATTAA	1860
GGGAGAGCAT ATTGGGTGAT GTAGGGAGG AAGAAGAATG ATGTCAAGAT TCCCAGTTGG	1920
GGACCTGACA ACATTGCAAC ATAAGACACA CAAGAAGATC GGTTGGGTGG CTCATGCCATA	1980
TAATCCCAGC ACTTGGGAG GCAGAGCCAG GAGGATCACT TGAGCCCAGG AGTTCAAGAC	2040
CAGCACAGGC AACATAGTGA CACCTCATCG TTACCCAAAA TAAAAAAAAA AATGAGGTGG	2100
GAGGATTGCT TGAGCTCGGG AGGTTGAGGC TACAATAAAC TGTGATCATG CCACTGCACT	2160
CCTGCCTGGG TGACAGAGTC AGACCTGCC TCAAAAAAAAAA AAGACACACA AGAGAAAAAT	2220
ATCAGCGTGT TGTTGTTT TCGTGGAGTT AATTGTGGGG TTCTAGGGAA AGGAATTAG	2280
CTTGGGACAT GGAAAGTTG AGGTTCTGT AGAGTGTCCC AGTGAAGATT TGTAAATAGAG	2340
CATCGGATGC GCATATTAGA TGGCACTTGG TGATATGATA AGAACTCAAA AAATATTGA	2400
GGAATAAAGG AAAGAAGAGG CCAGACGTGG TGGCTTATGC CTGTAATCCC AGCACTTGG	2460
GAGGCTGAGG CAGGGGATC ACTTGTGGTC AGGAGTTCGA GACCAGCTG GCTAACATGG	2520
TGAAAAACCA TCTCTACTAA AGATACAAAA ATTAACCGGG GATGATGGTG GGTGCCTGTA	2580
ATCCCAGCTA CTTGGGAGGC TCAGTCAGAA GAATCGCTTG AACCCAGGAG CGGGAGGCTG	2640
CAGTGAGCCG AGATCGCGCC ACTGCACTCT ACCCTGGCA ACAGAGCCAG ACTCCGTCTC	2700
AAAAAAAAAA AAGTGAGAGA GATTGAGGCT GGGATATATG GCTCAGGCAT CATGCGCGTG	2760
TAGGGGCCAG TTAAAAAGCA GAAGTAAGAA AGATTGCCTA GGGAGGCAGG AAGGGTGAGG	2820

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TGAGAGGAGA AGAGGCCAG GACCAGATT TAGTCACCAA CAGCGTTAA GGGGCAGGTA	2880
AGGAAAACAA AACCATCAGC AAAGACTGAG AATGAAAGCC CAGAGAGGAA GGAAAAGCCA	2940
CACATACAAT CAGTACAGCT CCATCTGAAT AAAGGTAGCG CCCCCCCCCC CCCAAATCAT	3000
TAGAGAAATG CCTGATTCGG TTTCTGTGG ATTTTCCTA AGAACCTAGA TGTGGGAAT	3060
AGAAATAAAAT GGTTCCCTCT GTCTCATCCC CTCCCTGCC TCTGAGAGGA AGCTGTGATT	3120
GCGTGCTCCC TTTCTGGGG TGCGAGATACT TTCTGGACCA ACCCTCAGTA CCGTCCGAAG	3180
CTCCTGGAGG AGGACGATGA CCCTGATGAC TCGGAGGTGA TTTGCAGCTT CCTGGTGGCC	3240
CTGATGCAGA AGAACCGGGG GAAGGACCGG AAGCTAGGGG CCAGTCTCTT CACCATTGCC	3300
TTCGCCATCT ACCGAGGTGTG TAGTCCTGAT TGGCTCCAGC CCAGGAAACA TACTTCCC	3360
GAGAGGACCC TTCCAGGGGC TTCTAGAGGG GCCCTCTGCT TCCTCAATAC CAGTGACCCA	3420
CAGAGCTCCT GGTATCAGGA CCACTGTGT TTGTAACAAG CAAAAAAATAC CAGGGGGGGC	3480
ATTAGAGAGG CAGTGGAGGG GGCCTGGCAG AACAGGTGCC TGGGGTCAG GCTTCCGCAT	3540
GGGGGCTGCA GTTGCTGGCA TTGCCTTCCG CAGGCTCCTC ATCCTCATTG ACATCTGAAG	3600
CATCTTCCTT TCTGTTCTT CTCAAGGTTT CCAAAGAGGT ATAGCAGGAG CAGGGGCCAG	3660
CAGTTGTGTG CAGCACTACC CAGGGGGGCC CGAGTCTGTC TGTGGCTCGT CGAGAAGCTT	3720
CCTGGTGGGG TTTGTGGCA GGACTTGTGA TAGGAGAGGG CCTTGCCTGT TGTTATTCC	3780
CACTTGCAGA GCAGGTTGCC TCAGGGCATT GCATGACCCA TGACTACCAC CCCCAGGATG	3840
TGCACTTCT CCCTCGCACC AGACACTGCA CGTCACACAC ATGCCCTTGC ACACTCACCC	3900
TCCTCCACGC TTACAGCCAC ACACACAGTC ACACAGACCC GTTCTGAGGG TGGCTCCCCG	3960
CTTGGGATGG AGGAATCACT TCCCTCAGAA CCCAGCCAAG TCCTCTAGGC CTCCCTGGGG	4020
GTCCTTCCAG CCTGAGGGGC TTGGAGCTG AGGACAGCTG TTCTGCTAAG TGTCCCTGAG	4080
TGTGGGATG ACACATTTC ATTCACTCTG AATCACAACA GAAAAGGGAA GAGGAATTGA	4140
GGTAGGGAGC CTATTTAACCTTGGAGTC GGGAAAGTAGG GAGGTTGAAA CTGTGACATG	4200
GGTGACCAGG GAGTTGGAA GGGACCCCTG GAGGTGGCTG TGGCAGGACA GGACGTTCC	4260
CCCCAGGGGC TCATGTCCCC TGGGCTCTCC CCATCTCTCA GATGCACGGG AACAAAGCAGC	4320
ACCTGCAGAA GGACTTCTTC CTGTACAACG CCTCCAAGGC CAGGAGCAA ACCTACATCA	4380
ACATGCGGGA GGTGTCCCAG CGCTTCCGCC TGCCTCCAG CGAGTACGTC ATCGTCCCT	4440

FIG. 8D/3

SUBSTITUTE SHEET (RULE 26)

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CCACCTACGA	GCCCCACCAG	GAGGGGAAT	TCATCCTCCG	GGTCTTCTCT	GAAAAGAGGA	4500
ACCTCTCTGA	GTGAGTGCTG	GCCCAGCTTT	CCCACGTGTT	TCTAAAAGCT	CACATGGCCC	4560
ACTCCAGAGG	TTGAAGGCAT	GAGGCAGCTA	GACACGTCTC	CTCCAGGGTC	CTTCTGCTGC	4620
TCCTGAGCCA	CTGGCCACAT	TACCCCCATT	CATTCAATTCA	TCCATTCTGT	GATATTTATT	4680
GAGCACCTAC	TATGTTCCAG	GCACTGTCCT	AGGCACTAAG	GATAGAGTAG	TGAAGTAAAC	4740
AGAAAGAAAT	CCCTGCCITC	ATGGAGCTTA	ATATTCTAAC	ATGAGACAAT	AATGGATAGG	4800
AAAAACATAT	GTAGCATGTT	AGATTGGAG	AGGTGATATG	GAGCAAAAT	AAAGTAGGGA	4860
AGAGGGATAG	GAGGTGTTGG	GGATGCTGA	AATTTAGGT	TACCATGGCC	AGGAAAGCCA	4920
CATCCTGTCC	CTGGCCACCA	CAGATGAGCT	CATAGCCCC	GCCACTCTGA	TCTCTGTCCT	4980
TGGAAGATGC	ACCAGGTCCA	TGGTAGGTG	GCTGGTCAT	GCCTTGGGG	GGCTCTGAGC	5040
AATACTAAC	AGAACCTGCG	TGCCTGGCT	TGGCTGTGG	GGATGGTGCT	GACATGGGGC	5100
TGGTTCTGG	GGTGGGGTG	TTCCAGGGGT	TCTCTAGAGG	CTGGTTCTGG	CTTGGCTGCC	5160
AGGAAGCCGT	GCACCAGAGC	AAACCGTCCA	CGGGCCTCCT	GCTTGCTTCT	GGTGACACTG	5220
AGACCCACA	TGTCTGTATT	CCTCACAGGG	AACTTGAAA	TACCATCTCC	GTGGATCGGC	5280
CAGTGGTGAG	TCGTTTAGAT	CTTCTGTGCC	AAAAGTCCAG	AGGGTCCCCT	TCCCTGACCA	5340
TGCAGGGGAC	AGATGGTGCA	GGGGAGAATG	GGCACTGGCA	GAGGAATGG	GAGTCTGGC	5400
TGTGCTGAGC	AGTCCCTCCT	TGGCACTGCA	AATCCTACTT	TGGCATGGCC	AGAAGTAATC	5460
GGCCTTAACC	ACCGGGGGCC	ATTGAGGCAG	TTCAGGGCT	GGGAAATATG	GAAGAGGGTC	5520
CTGGAAAGGA	GAAGCAATT	GAACAATCGG	AGGAACAAG	CCCACAGGAA	GGGATGACAA	5580
GAGCCGCAGC	GAACACTGGA	TTCTGAGACT	GGATAACATT	GGATTCACA	CATAGAGAAA	5640
AGAAAGTAAG	CTGGTGCCGG	ACCTGGTGT	GACACTTGGA	TCCTCCACTT	ACCAGCGGG	5700
TGACCTGGAC	AATTCTGTA	ATCCCTCTCA	CTCAGTTCC	TACTCAGTAA	AACGGGGATG	5760
ATAATGTGCC	TTGCAAGGCT	TTTGTGAGGC	TTCATCAATG	AGGTGATGTA	TGTGAAGTGT	5820
CTGGCACAGC	ATGGGCACTC	AAACAGAGGT	GCTTTTCAC	ACTTACACC	TTACAAGGTA	5880
CTTTACAT	GTGTCATCGC	GATACTTGC	AGGTTGCTGA	GAGGTAGATG	GGGTTATAAT	5940
CCCTGGTGT	CAAGAAAGGA	ACCAGAGGCT	CAATGGGGTT	GAATGACTTC	TCTGACTTCA	6000
CAGAGCTCAG	TAAGTGGCAG	GGTTTGGAAC	TCACATTCA	ACTCTCTGAC	TCCAGACTTA	6060

FIG. 8D/4

SUBSTITUTE SHEET (RULE 26)

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GGTTTTCCG CACCTCCACG CTGAGGCCAG CCCCAGGCAG TGAGAAGCCC AAAGTCCGAA	6120
GCACAGAGTG CTGTGTGTTG GGCTCTGTGT GTTGAGGAGT CTTGTGACTG CCTTGGGGCT	6180
TTGGGCTGTA GTCAGCTGAC AGTCCTTGT GCTCTGTGGG GATGACGTAG GCCAATGGGA	6240
GGACAAATGC CCCTCTGAAC TGTCTTCTGG GCAGTGACAG TCATGGTCAT AATCCTGACC	6300
CTGAGCCAGT GCCCAGGTCTC CAACTGCCTT CTGAATGACC ACAGGCGATT GGTTTAGTG	6360
GTAGGTGCGT GGGGATCTGT TCTGGTCATC TGGATGCTGG TCATCGGGTG CAGTATTGAT	6420
CAGGACCTGC AAACCCAAAA GCTTATGGGA GCTGGCACGT CACGTGAGTA GACCAGGCAG	6480
GTGCAGGGTT TTTGATGTCC CTGCACTGAC ACAGTTGTCT GCAGTTCTCC AATTGACAT	6540
TTGGGCTCCA GTGTCGAGGG TCAAACAAGG AATTTTGGGG CGTGGGCCAA ATCTGGGAAG	6600
ACACAGGGAG CAGGGCCCTT TGGCTCAAGC TGATAGTTGC CGCAGGGATT ACCAGGCCA	6660
GGGCAGCCTG CCACAAGCTG GGGCTTTAC CAAAGAAAAT CTCCCTATGT TAAATGCTTG	6720
CTCAAAAATT TTAAAAAAAT ATTCTGTAAG TCAAAATCCA TTGTTAGGTC AGTTGAGAG	6780
ACCCATGTTT TTGGTGTTTT ACTAACCAAT TTCATTTTT TATTATTTAT TTATTGTTT	6840
ATTTTGAGA CCGAGTTCA CTCTTGTAC CCAGGCTGGA GTGCAATGGC ATGATCTCAG	6900
CTCACTGCAA CCTCCGCCTC CCGGGTTCAA GCAATTCTCC TGCCTCAGCC TCCTGAGTAG	6960
CTGAGATTAC AGGTGCCAC CATCACGCCCT GGATAATTIT TGTATTTTT AGTCGAGATG	7020
GGGTTTCACC ATGTTGGCCA GGATAGTCCT GAACTACTGA CCTCAGATAA TCCGCCACC	7080
TCAGCCTCCC AAAGTGCTGG GATTACAGGC ATGAGCCAGC ACGCCCGGCC ACCAATTCA	7140
TTTTTAAAAA AAGGAAGAAA GAAAACCTTA GCCAGAAGAT CTTTTCTT CCCATATGCA	7200
GTAAGAGTAG ATTATAAAAA CAAAGTCAGA GCAGTCACTG GTGCTGGGC ATGGAGGAGA	7260
AAGAAGAATT CTCTTCTCCC TTCACCCCTCC ATGCCCTTT TTGGCTCCAT GTGATTCA	7320
TTTCTGGACC CTGGAGCCCC ACCCCAAGCT AAAGACCAGG ATACAGGGAA GCCACAACCA	7380
CTGGCGGTTC TGAGAACTTA CTTTCACCTT ATTCTGCATT TACTGTTCC TTTCTTATG	7440
CAGAAAAAGA AAAAAACCAA GGTAGGTGTG TGGGTAGAGA GCATGAAGTG TGTGTACTCA	7500
TGCATATGTA TGTGCATGCA TGTGAAGTGT GCATGTGTGA GCTCATATGC ATCCATGCAC	7560
CAGACTTGCC TCTCCTCCC CCTCCTTCCT GAGCTTCTGC TGGGCCGAG CGTGCAGTAA	7620
TGACAACTAC GATTTGCTGG GGGAAAGGCTA CGTGCCAAGC ACTCTTTAG GTGCTTCCA	7680

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TGATTAATTCTTCCTCACA ACAGCCCTAT GAGATTAGTA CTATAACTAT CCCCATTTC	7740
AGAGGGAGAA AAGGTACAGA CTTGACTAAC TTGCCAAGG CCACACAGCC AGAGAGGGC	7800
AGAGCCAGTA CTTAGAGCCA GCCAGTCTGG GTCCAGAGTC CGTGTCTGA ACCACAAGAG	7860
GCCATCATAC GCCATCAGAT TTGGTGCTAG CATTCTGGT GGTGCCTGGT GGTGATGGAT	7920
CCATCACAGG GGTCTCCAG GTACTGGTGC TGGCCCAGAC CAGAGCTGAC ACTCCTCAGG	7980
CACTACCACA TTCCAGGCAC TGTGCTTGGG GTCACTCCCT CTCTTTTTT TCCCCCCCAC	8040
TTATAACAGT ATCTACAAAG TAGGTGCTGT TATTTTCCC CTTTCACAGG TGAGATAGAC	8100
TCAAAGAAGT GAACTTGCCC AAGGAACACA ACTAATGAGT GGGAAAATG GAACTGGAAA	8160
CCATGTCGTGTTACTCCAAA ACCTGTGTTT CTTGCCCTCT TTCTCTGATG CCAGCCCCCT	8220
ACACTTCAAG GCCTGTGTTG TCCAGACCCA CACTCGGGCC TGCCAGTGTG TGCTGGCAG	8280
GGATGCTCCA TGGCCACACC ATATCCATCC TACACATCCC CCCTCAGACT GTGACCTCCA	8340
TTTGCTCTGG GATCCCCACA AGCTTCAGCT GCTTGACCAA GACACTGCTT AGAAGGCAGA	8400
GCAAGCCAAG GCCTCTGGGG CCTGCTGGGA GCCAAAGCTG GGGAGCCGTT TCCACGGGTC	8460
TATCTGCTTG ACCTGTCTTA GATGAGCAGC ATGGAAGGGC AGTGGTGCAT GAGTCCAGGC	8520
GGGCTGCTTT TCTGCTCCGA GAGGCTCTGC CTGCCAGTT CTTCTCTGCA TTGCAGCCTC	8580
AATCCCCACA GCCTTGCTT CCCCCGGCTT TCCCTACAGG TGCAACGGCAT CCACAGTGTT	8640
GGCACCATGC ACCAGCCGCT CTCCGCTCTT TTCATATCCT TGTCACTTGC ACGAGCATGT	8700
CTTGAAAATA TCCCTTGTCTT GTCTAGCATC TTAAATGTTT TTGCACTATG ATTTTGCATT	8760
CAGTATCTCA TTIGATCCCC ACAAGAGCCC TATGAGGAGG GAAACCGAGAT TTTACCATTA	8820
AAGGATGAGT AAACTGAGGC CAGAGAGGAT ATTTTGTTT TTTTTGAGA CAGTCTCACT	8880
CTGTCACCCA GCCTGGAGTG CAGTGGCTTG ATCTTGCTC ACTGCAAGCT CCACCTCCCA	8940
TGTTCACACC ATTTCTCTGC CTCAGCCTCC CAAGTAGCTG GGACTACAGG CACCCACCAC	9000
CACACCCAGC TAATTTTTT GTATCTTAG TAGAGATGGG GTTTCACCCA GTTAGCCAGG	9060
ATGGTCTTGA TCTCCTGACC TTGTGATCTG CCTGCTTCCG CCTCCTAAAG TGCTGGATT	9120
ACAGGGGTGA ACCCCCCCTGC CCGGCCAGAG AGGATATTTC TTAATGAGGG GCAGGGCTGG	9180
GATTCCAGCC CAGTGTCTG ATGGCTCACC CACTGACCAT TCCACTAATC CGTGTCTTT	9240
TTCAATCTAA ACTTCAGGG TTGTAGAGGT TCCTTGAGG TGCTCAGTA CTTCCATGGT	9300

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GATGTGGGTT	CTGAGGGCCA	AGAGCTCTGT	TCTCATTAAT	CAGAGAAGCT	TGTGTTTTA	9360
AAAACACCAT	GTTCAGTGCA	GGAAATTAA	TTGGACAGTG	TTTCCATCTG	AAAAAAA	9420
AGTCTACAAA	ATACTTGACA	ATCACTGCAC	TAGATCATGC	TGCTTTAGC	ATTCTTAGCA	9480
TTTCACGTGC	TGAGCTCTCA	ATACTCTACC	ATGAGGAGGG	ATGGAGTGGG	TATGAAAAGA	9540
TAAAGAACTG	AAGTCACACCG	GCTTGTCACT	GGCAGAGATA	GAGCTTGAAC	CGAGGTTGAA	9600
GAGCTCCCGC	CTATTCCTTT	CCTCTTCTCA	CTGGATAAAAG	CTGCTCCAAG	AGAGGTGCTG	9660
CCTCAGTGTG	CCTGTTCAGA	CTGTAATCCT	CCCTTCCCTTC	CTGCCTCCTC	CCTCCCTCT	9720
CCAGCCCCATC	ATCTTCGTTT	CGGACAGAGCC	AAACACCAAC	AAGGAGCTGG	GTGTGGACCA	9780
GGAGTCAGAG	GAGGGCAAAG	GCAAAACAAG	CCCTGATAAG	CAAAAGCAGT	CCCCACAGGT	9840
GTCTGGGCAT	GTGGCATGGG	TGGGTGGCC	ACCACGCTAC	AGGGGCTTCC	TATGCCCTTG	9900
GGATACACAG	GGGCTGGAGG	CTTCCCAGGA	TTTGTCTTG	AACATCTGGA	GGTTTGAATT	9960
TGTCCCAC TG	ACCTTTCTT	TCAGCAAGTT	CCCCTGAAAT	TTGGGCTGCT	GCTTGGGTGA	10020
ATATCCCAGG	ATGGGGGTTTC	CATTCTAGGA	GTGGACTGGC	AGGCTGAGCC	TCCCATGGAG	10080
CTGATCCAGC	CAGGATACAG	AGAAGGGAG	GCAAAGGCTG	AGACAGAAC	ACCTTGAGAG	10140
CGGAGGGCGA	ACTCTTGCT	CCTGGTGGCC	TTGAGCATT	CACAATAGGG	GGATAAAGGA	10200
TAGGAGCAGA	AAAGTGGGGC	TGACTTCAGA	AATGGGGTCC	TCTAGAGCTC	ACGGGAGGGT	10260
GTTAGATTGG	AGTGGGAGCT	TAGTGGAGGT	GAGCCTTACA	GCCAAAAGTC	TCCAGACCAA	10320
TCCAGGCC	CTCTTCTATC	CGGGGGCCCC	TCTTCTATCC	AGGGCCCTC	TTCTGTCTGG	10380
GAGCCCCCT	TCTATCTGGG	CCCTCATGCA	GTGGGGCCTA	GGGGAGGTT	TCTGAGGACT	10440
TGGCCTTGAT	GACAGGGTGG	CTGGAGGAAT	CAGAACGGTC	AGACCTTCTT	TGACCTGCGG	10500
CCACCTT	TTGGAATGCT	CAGGCCTGGG	ATGGTGGAGG	GGGCTCTTGC	AGGTGGGGAC	10560
TGGGTTGGCG	GGGAGGAGGC	TGTATGGCCG	CCATATCTCC	TTTGGCTGGG	GGCGTCAGGG	10620
CTGGAGAGGT	GTGAAGAGTC	CCTGAGGCCT	CGATGCATCT	CACTCCAGCT	CACCAGGTCT	10680
GCATTTGCC	GTCCCCAGCT	CCTGCTGCCA	CCCCCGGCCG	TTTACGGCAC	TTGGCTCCCT	10740
TGGCCCAGAG	GAGCTTGCCT	CACAGGCCTG	TGCACCTCTG	ACCCCTGTGA	ACCAGTTTC	10800
CTTTGTGCCT	CCACAGCCAC	AGCCTGGCAA	CTCTGATCAG	GAAAGTGAGG	AACAGCAACA	10860
ATTCCGGAAC	ATTTCAAGC	AGATAGCAGG	AGATGTGAGT	ACCTCCAAGC	CCAGGACGCC	10920

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CACAGGTGCT TCCTTCTCTC CTGGATTAAC TGCTCAGATT ACCAATTATT TCATTATTGT	10980
TTGGTAGAGG TCACTTTGGA CTTCGGTGGA GCCAGGGGAT GTGTGGTAG CACACAAATC	11040
CACAAGCCCT TGAGTTTG ACTGCCACGT CTGCTGGGG GCTCAGAGGC CTTTTGCTC	11100
TGAGCTGCC ACAGTGGTCC TGATAGCTGA GGTGCAGTAT CTGGCCCCCT GTCTTCCTCA	11160
GAAAAGCCCC AGCTTCCCCT GACATAATAG CACCGACAGG GATTTACAA ACACAGCCAG	11220
GTGGAATTG TTTTGCAGAAC TGTCCCGGCC AGGAGCTGCT GTACTCCTGA ACCATGACCC	11280
TCCTCTCCCT TCCTCCTCAG GACATGGAGA TCTGTGCAGA TGAGCTCAAG AAGGTCCCTA	11340
ACACAGTCGT GAACAAACGT GAGTTGCTCA AACCAAATGG GGGTGGGGTG GGTGGGGAGT	11400
CCCGTTGTCT CAAAGCAGCT CCTCACTCTT CTCCATCCCC CCAGACAAGG ACCTGAAGAC	11460
ACACGGGTTTC ACACTGGAGT CCTGCCGTAG CATGATTGCG CTCATGGATG TATCCTTCCT	11520
GCCGCCCTT CCCGACCCCTC TGTATCAGC CCACGGGGC CAAGGCAACA TACAGGGTGC	11580
CCAGTCAGGC AAAGGGCCCT AATTTGTGCC CAGGGAAACT TAAGGAGACC CTGATTCTAGA	11640
ACATCTTGGAA TACTCGTCTG AAAGGGTTG TTAGAGGCCG AAGGGGAGGA TGTTGGGTTG	11700
TAACTGCCCT AACCCCTGTG CTTCTCTCAG GCCTGGGATC CTGCCCAACC AAAAGTGGTC	11760
CTTAGGAGAG CGGCTCCTGG GTTACAGAGT AGGCCAATC TCTGACTGGT GGTGGACTGG	11820
AGGGGAGGGT TAAATAGTAC AACAGGGCAG TGGTAGGAC AGCCCGGAGT CTCCTAGACC	11880
CTCCCTCCAA ATCCAGGGGG ATTTGCTGT GTGCTGTGA GCCCTGACCT CCCTCCTCCA	11940
GACAGATGGC TCTGGAAAGC TCAACCTGCA GGAGTTCCAC CACCTCTGGA ACAAGATTAA	12000
GGCCTGGCAG GTGGGAAGAG AAAATGAAGC GTGGGAGTCA AGAATGGGT TGATTGGAG	12060
ATTCACTGTG TGACCTCCAT CCTCAAATTT TCTATTGCCA GAAAATTTTC AAACACTATG	12120
ACACAGACCA GTCCGGCACC ATCAACAGCT ACCAGATGGG AAATGCAGTC AACGACCCAG	12180
GTGCTGAGAA GGAAGGGGTG TCAGGGATGT GGACCCGAGA CGGTGGGAGC AGGAATGGGA	12240
GGGGACTAGC TACTAGGGCC CCACTAGAGA AGGAGAGGGA AAGGGCTTCT CACTTTCCCT	12300
TCCCAGGTCA CAGAGTGTCC GAGAGGCAGG GAAAATAGAA GACAGGCCCA AGGCCTCCAG	12360
CTCCACGTCC ACCTCTAACCA TGGTCCCTC CACAGGATTG CACCTCAACA ACCAGCTCTA	12420
TGACATCATT ACCATGGGTT ACCGAGACAA ACACATGAAC ATCGACTTTG ACAGTTTCAT	12480
CTGCTGCTTC GTTAGGCTGG AGGGCATGTT CAGTAAGTGG GAGAGGGGG CTGCCCTCTG	12540

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CTCTCTTGCA GGGCAGTTG TGGCAACAGG CATCTCACCT GATAATCTCC AGTCTGCTCC	12600
ATCCAGGCTG AACAAAGGCC AATGACCTCT TTAGGCCAG AATGGATGG CAAAGGGAGG	12660
GTTACTGGTG ATTCTCTGCC TGACACATCTT TGTGCTGATG AGGGACAGCA CTGGGCACAC	12720
GGTCCTCTGA GGGGAAGTTA CAGTAGTAGA GGCGGAGTGC GCCTGTAACG GGCCTCTGGC	12780
CTGTGCATTG TTTCACAGGA GCTTCTCATG CATTGACAA GGATGGAGAT GGTATCATCA	12840
AGCTCAACGT TCTGGAGGT AAGCATAGGC ACAGCACATT CCCCTACAC ATTAAAAC	12900
AAGGTGGAGG GGTCAACGGG GCGGACTGGA CCCAGGGTGT GCTCCTCATT TCCACACAGT	12960
GGTGGACGGA AGGGATAGGA ACAGAACATG GAGGGAGGCT CAGCAGGCTC CCAGGACACA	13020
TGCACTTGAG GCCCAAAAGG ACCTCTGCTC CCCCAGTCAC TTGATGCGGG AAAACATGCA	13080
CCTTCTTAGG GAAGATCTAG GAGAAAGGAA ACAGTAAGCC ACTGCTTCTT GGAAAATCTT	13140
CTGGGGGTCT GACCTGCTGG GACTGTTCCC TTTCCTCTTG CCCCGTAAGA TTCCTAGGGC	13200
GGGGGGGGGG GGGGGTCACT CTTTCTGAT CTACATTCTG ATCTTGGAC TTCTTTCAGT	13260
GGCTGCAGCT CACCATGTAT CCCTGAACCA GGCTGGCCTC ATCCAAAGCC ATGCAGGATC	13320
ACTCAGGATT TCAGTTTCAC CCTCTATTTC CAAAGCCATT TACCTCAAAG GACCCAGCAG	13380
CTACACCCCT ACAGGCTTCC AGGCACCTCA TCAGTCATGT TCCTCCTCCA TTTTACCCCC	13440
TACCCATCCT TGATCGGTCA TGCCCTAGCCT GACCCTTAG TAAAGCAATG AGTAGGAAG	13500
AACAAACCCCT TGTCCCTTTG CCATGTGGAG GAAAGTGCCT CCCTCTGGTC CGAGCCGCCT	13560
CGGTTCTGAA GCGAGTGCTC CTGCTTACCT TGCTCTAGGC TGTCTGCAGA AGCACCTGCC	13620
GGTGGCACTC ACCACCTCCT TGTGCTAGAG CCCTCCATCA CCTTCACGCT GTCCCACCAT	13680
GGGCCAGGAA CCAAACCAAGC ACTGGGTTCT ACTGCTGTGG GGTAAACTAA CTCAGTGGAA	13740
TAGGGCTGGT TACITGGC TGTCCAACTC ATAAGTTGG CTGCATTTG AAAAAAGCTG	13800
ATCTAAATAA AGGCATGTGT ATGGCTGGTC CCCTCTGTGTT TTGTTGTCTC ACATTTAGAT	13860
ATCAGCCATG CATGACTGAA TGGCTTCCAA TCATATACTC ACCTATCACC TACAAGAGAA	13920
CAATGAAAAA CACACACAAA AACAAAATCT TGAATTTGT AATCATGCCT ATTGCTATTT	13980
CTTGAGCATA AGAATGGCTC AGATACTTTC CAAGACATAA AAGGAAGGCA GAGGAATAGT	14040
TGTTGCTGTA AAAGACATCA AGAATAAATG GGGTCATGTA CAACGGGAGG GCCCGGTTAC	14100
CTGAATAATG GAGTGGAGAT TGAGCTATCC TAGCTCCTCT GCTCACTAAC TGACCTGTCC	14160

FIG. 8D/9

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CATGACCGTG GACAAAACCC TGAACGCAGC TGTTTGTITG CTAAACTTCT CTGGACCATG	14220
GCCTGCGGCA TATCTATAGG CATCCTGTGT TTTCCACCCA GTTTCCTTCT TCCTCGCTAA	14280
GCCAACGTGG AAAGGGCTGG CCGTGAATAT GCAGACAAGG TAACGAAAGT AAACCGTCAA	14340
TTAGTAAAAG TACTTCATTG TCCTCTTGTGTA TTTGCTTCAT TCTTGCTTCA CAAAGTTACG	14400
AAGTCCACAG CTTTATACCA AAATGTAAGA AGGCTATTG CTTATAAACCA TTTTGAGTCA	14460
GGTGTCACTT GATTTCATTC TTCTAATCCA TATTCAATAT TAAAAAAATCA GAAACCAAGG	14520
GTGCTGGAGC AGCTCTAGGG CATATATTTC TCTTAAATAG GAGAAAGATT TTCAACAGCT	14580
TTTCCTCCTT GACCCCCCTCC TTTCCCAATT TATTTGGGTC ACTACCTTGA ATTTAGAGTG	14640
AATCTGGGAA ATGTAGTCAC CAGG	14664

FIG. 8D/10

SUBSTITUTE SHEET (RULE 26)